

Fig 1

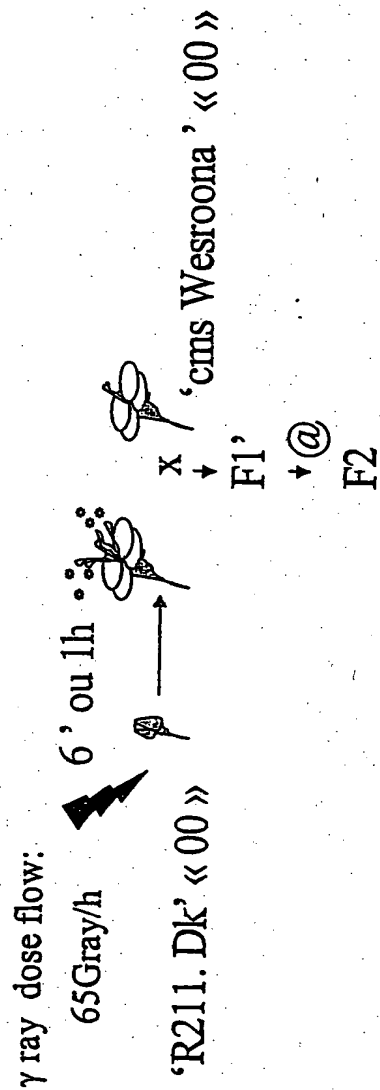


Fig 2

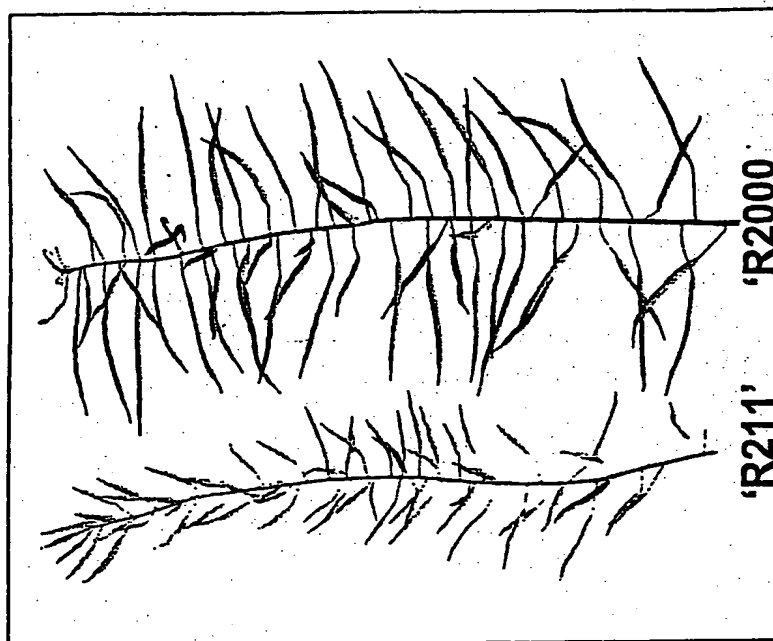


Fig. 1: Seed set on 'R211' and 'R2000'

Fig 3

Genotype	Selfings	Test Crosses
Drakkar	29.3	
Pactol	23.1	
R211	11.2	25.5
R2000	26.5 (24.0 – 31.1)	27.0 (24.0 – 28.7)

PGIBo1EH:AF258277
prIner-PGIINU
prIner-ant1PGLI
SGPiG|Chou
PGI-1DarrNEHAF258275
prIner-PGIU
SGrdr-saba Jo
SGrdr-aaba Jo
PGIBr-epaEH:AF258276
SGrdrInev
PGI-2DarrNEHAF258276
SGrdr-ar1ba
Consensus

PGIBo1EH:AF258277
prIner-PGIINU
prIner-ant1PGLI
SGPiG|Chou
PGI-1DarrNEHAF258275
prIner-PGIU
SGrdr-saba Jo
SGrdr-aaba Jo
PGIBr-epaEH:AF258276
SGrdrInev
PGI-2DarrNEHAF258276
SGrdr-ar1ba
Consensus

PGIBo1EH:AF258277
prIner-PGIINU
prIner-ant1PGLI
SGPiG|Chou
PGI-1DarrNEHAF258275
prIner-PGIU
SGrdr-saba Jo
SGrdr-aaba Jo
PGIBr-epaEH:AF258276
SGrdrInev
PGI-2DarrNEHAF258276
SGrdr-ar1ba
Consensus



Fig 5

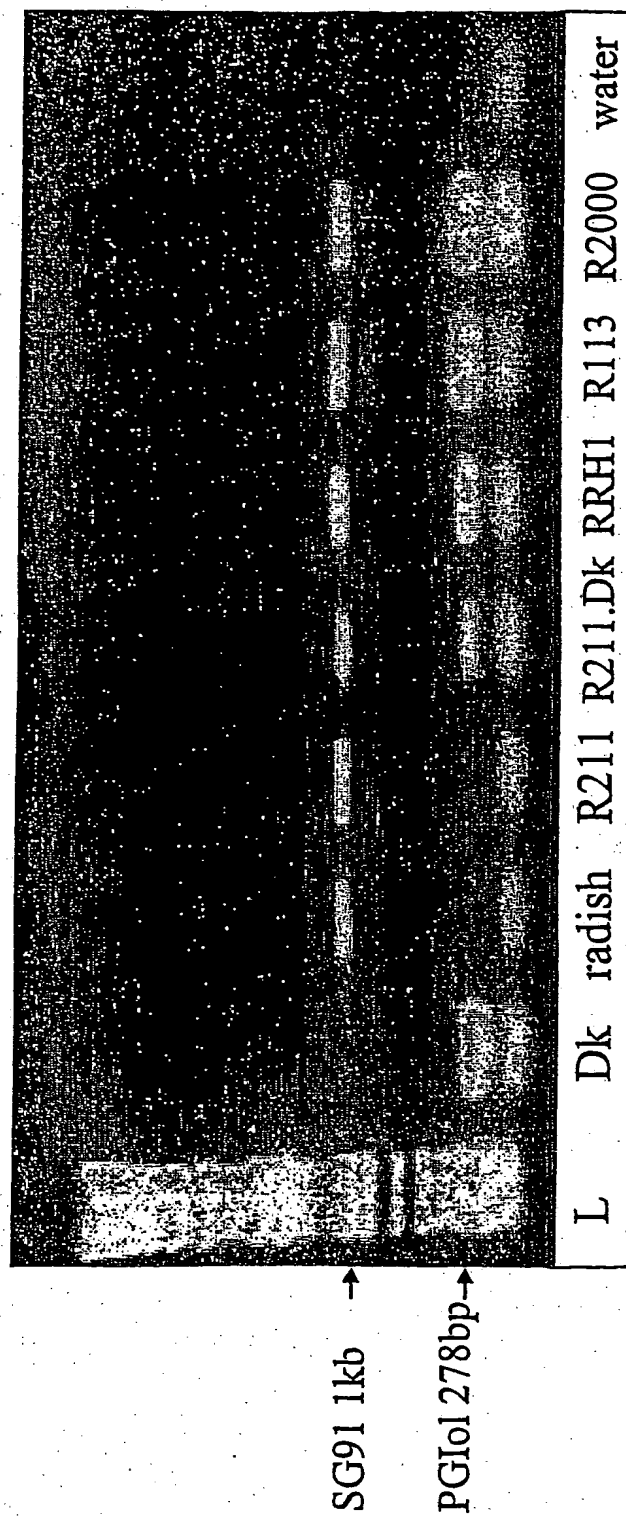
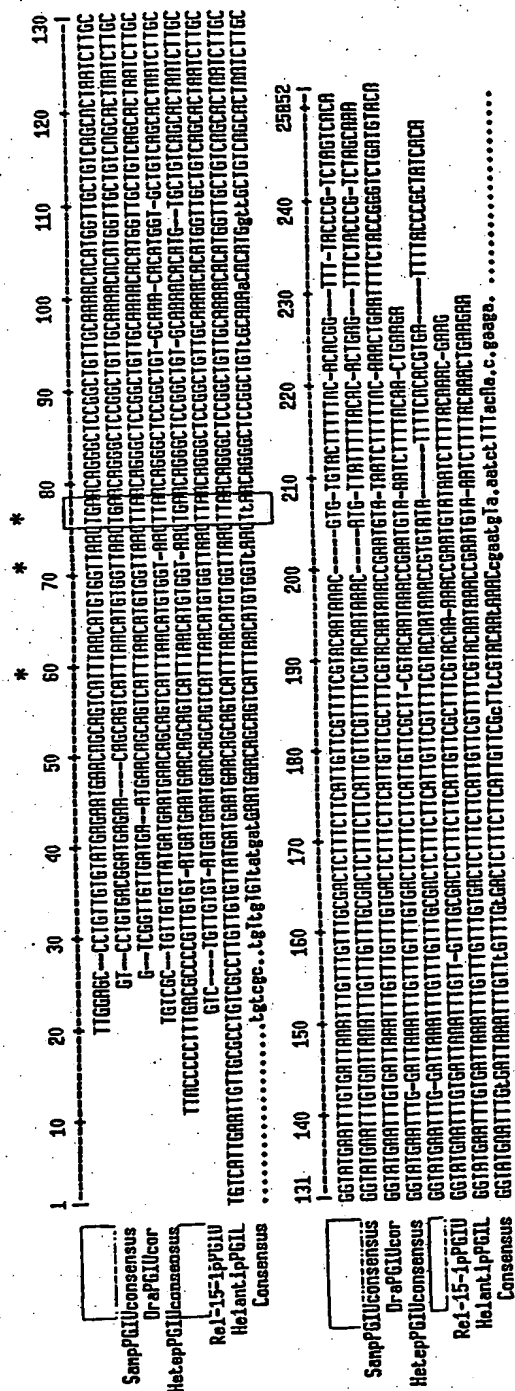


Fig 6



MseI restriction enzyme cut DNA sequences at the T/TAA sites (*)

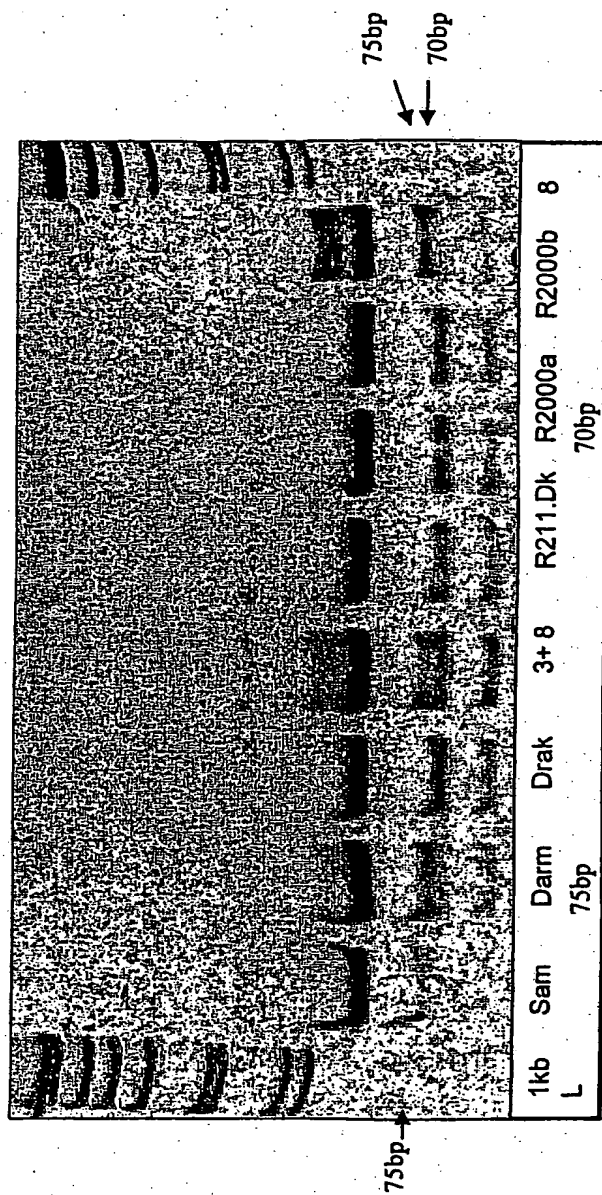


Fig 7

Fig 8

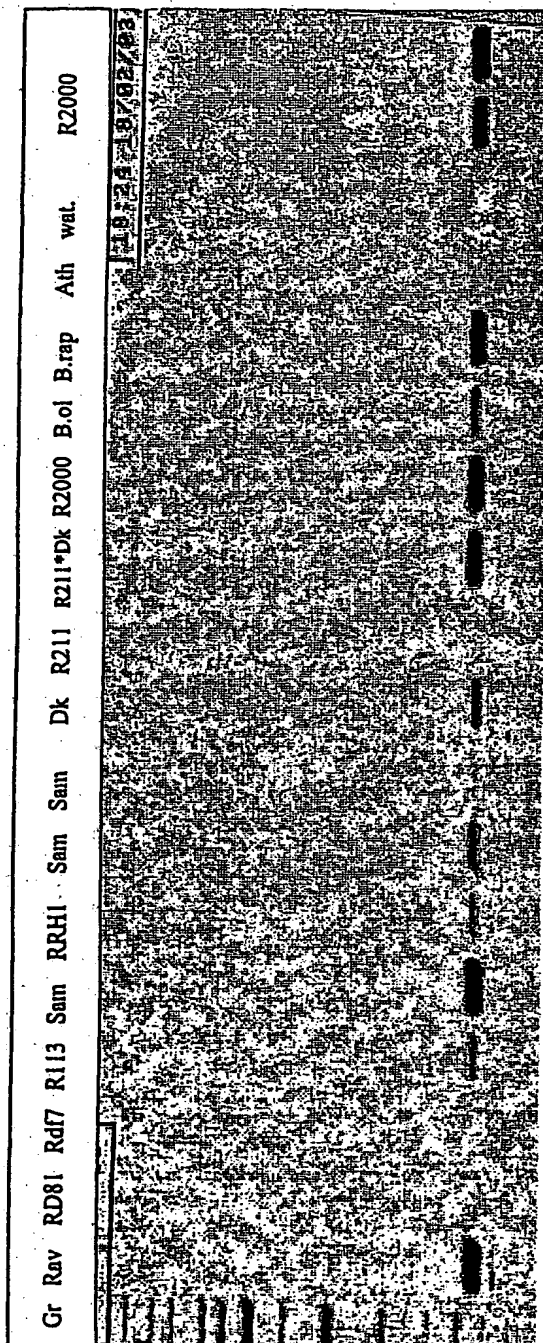


Fig 9

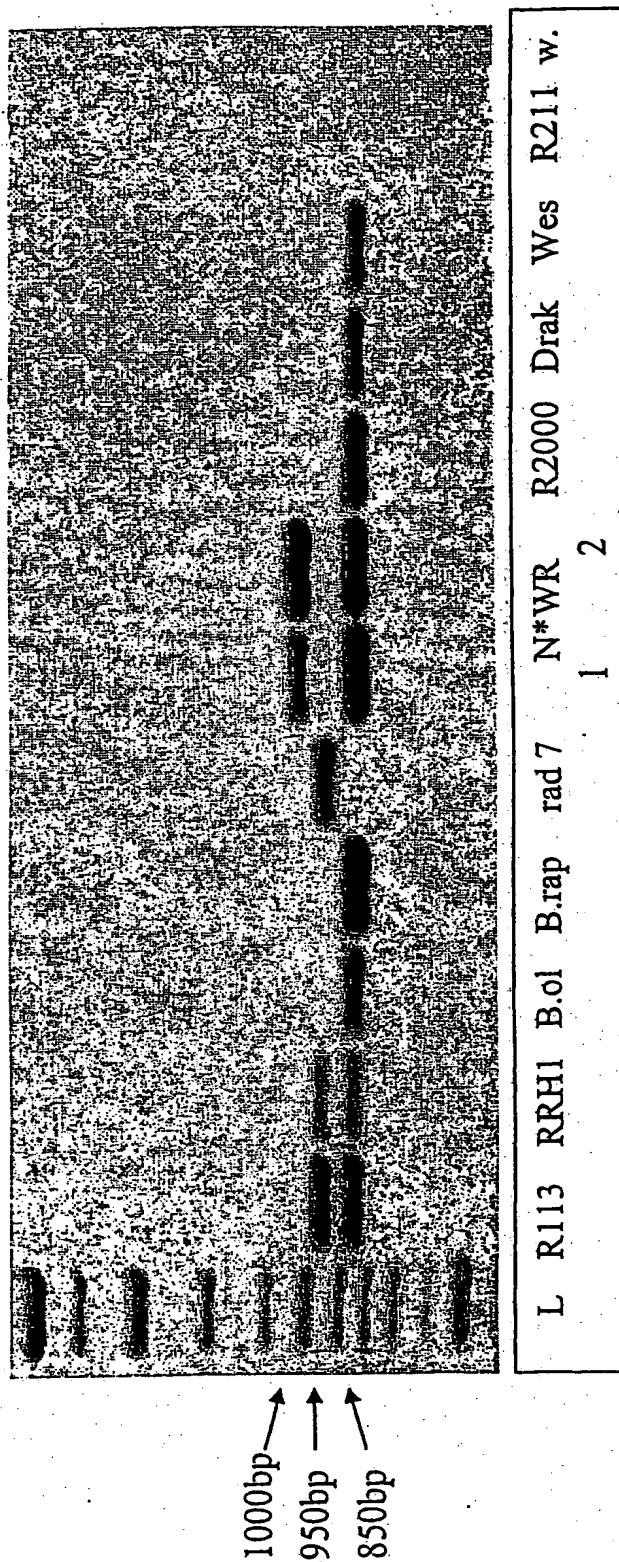


Fig 10

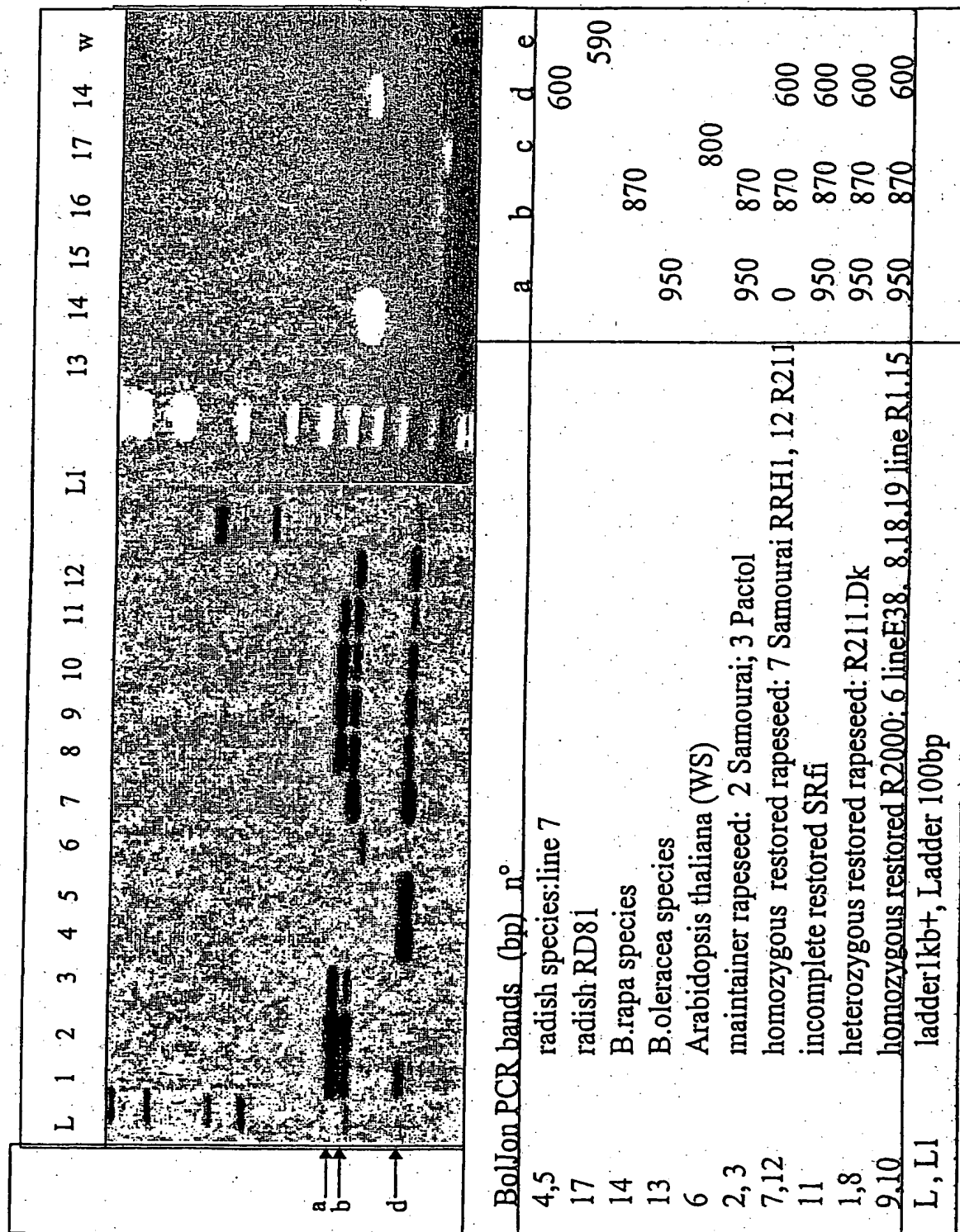
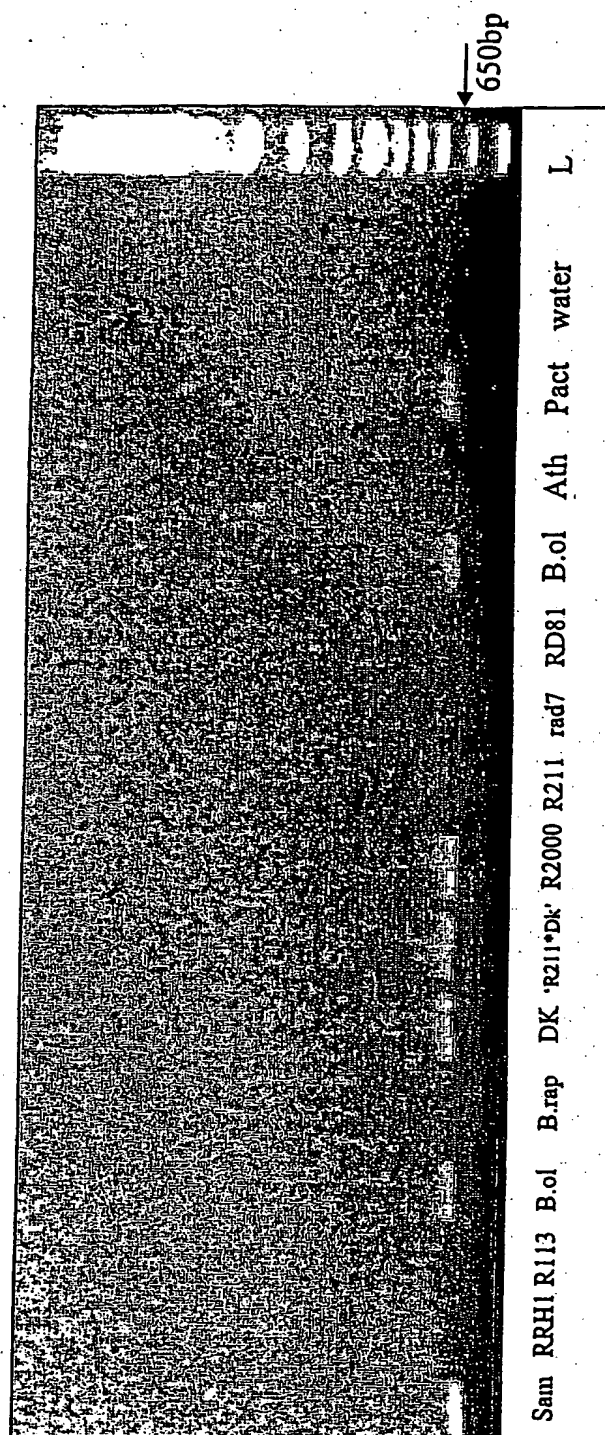


Fig 11



The CP418 band (about 650bp) specific to the *B. oleracea* genome.

It is present in B.ol, B.napus (Samourai, Drakkar, Pactol and the heterozygous R211*Dk)

It is absent from the restored rapeseed (RRH, R113 and R211)

It is present in the homozygous R2000.

Figure 13 (a)

	51		81 PGIol U --> 100
consePGIintUNTDrakka
consensWesrPGI
consePGIintUNTR113
consePGIintUNTBrapaA
ConsePGIintUNTRRH1
PGIBo-EM:AF258277	TTGCTTAGCG	TCCAAATTTTC	ATGATTGTAT TCATTGATT GTTGTG...
PGIBra-EM:AF258278	TTGCTTAGCG	TCCAAATTTTC	ATGATTGTAT TCATTGATT GTTGTGTGAC
consePGIintUNTBolera
consePGIintUNTR2000	TTG...	TCATT.GA...TTGT.TGCG
Consensus	1
	101	---	150
consePGIintUNTDrakkaGTCG	TTTGTGGTG AGT.GAACAG CAGTCATTTA
consensWesrPGI	GCCTGTTTG	TGTTATGATG AAT.GAACAG CAGTCATTTA
consePGIintUNTR113	GCCCGGTTGG TAT.GAAACG CAG.CATTTA
consePGIintUNTBrapaAG CAGTCATTTA
ConsePGIintUNTRRH1	CG TGTGAGAAG CAG.CATTTA
PGIBo-EM:AF258277	CCTG	TGCGCTTGTG TGTTA.GATG AAT.GAACAG CAGTCATTTA
PGIBra-EM:AF258278	TATCGCCTC.	TGCGCTTGTG	TGTTATGATG AAT.GAACAG CAGTCATTTA
consePGIintUNTBolera
consePGIintUNTR2000	CCTG	TGCGCTTGTG TGTTATGATG AAT.GAACA. CAGTCATTTA
Consensust.gg....t.gaa.ag cagtcattta
	151		200
		MseI restriction site	
consePGIintUNTDrakka	ACATG.TGGT	TAACCTAACA	GGGCTCCGGC TGTGCAAAA CACATGGTTG
consensWesrPGI	ACATG.TGGT	TAACCTAACA	GGGCTCCGGC TGTGCAAAA CACATGGTTG
consePGIintUNTR113	ACATG.TGGT	.AACTGAACA	GGGCTCCGGC TGTGCCC.. CTAAGGGTTG
consePGIintUNTBrapaA	ACATGGTGGT	TAACCTGAACA	GGGCTCCGGC TGTGCAAAA CACATGGTTG
ConsePGIintUNTRRH1	ACATG..GGT	.ACTGAACA	GGGC.CCGGC TGTGCAA.. .ACAG...TG
PGIBo-EM:AF258277	ACATG.TGGT	TAACCTAACA	GGGCTCAGGC TGTGCAAAA CACATGGTTG
PGIBra-EM:AF258278	ACATG.TGGT	TAACCTAACA	GGGCTCCGGC TGTGCAAAA CATATGGTTG
consePGIintUNTBoleraC TGTGCAAAA CACATGGTTG
consePGIintUNTR2000	ACATG.TGGT	TAACCTAACA	GGGCTCCGGC TGTGCAAAA CACATGGTTG
Consensus	acatg.tggt	taact.aaca	gggctccggc tgttgcaaaa cacatggttg
	201		250
		PGI int U -->	
consePGIintUNTDrakka	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTTGTGTT
consensWesrPGI	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTTGTGTT
consePGIintUNTR113	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTTGTGTT
consePGIintUNTBrapaA	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTTGTGTT
ConsePGIintUNTRRH1	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTTGTGTT
PGIBo-EM:AF258277	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTTGTGTT
PGIBra-EM:AF258278	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTTGTGTT
consePGIintUNTBolera	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTTGTGTT
consePGIintUNTR2000	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTGTTTGTGTT
Consensus	ctgtcagcac	taatcttgc ggtatg	aatt tgtgattaaa ttgtttgt
	251		300
consePGIintUNTDrakka	TGTGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC CGAATGTATA
consensWesrPGI	TGTGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC CGAATGTATA
consePGIintUNTR113	TGCGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC ..AATGTATA
consePGIintUNTBrapaA	TGCGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC ..AATGTATA
ConsePGIintUNTRRH1	TGCGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC ..AATGTATA
PGIBo-EM:AF258277	TGTGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC CGAATGTATA
PGIBra-EM:AF258278	TGTGACTCTT	TTCTTCATTG	TTCGTTTTTCG TACAATAAAC CGAATGTATA
consePGIintUNTBolera	TG.GACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC CGAATGTATA
consePGIintUNTR2000	TGTGACTCTT	T.CTTTCATTG	TTCGTTTTTCG TACAATAAAC CGAATGTATA
Consensus	tg.gactctt	t.cttcattg	ttcgttttcg tacaataaac cgaatgtata

Figure 13 (b)

	301		<---	PGIol antL 341		350
consePGIintUNTDrakka	ATCTTTTAC	AAACTGAA		TT TTCTACCGGG TCTGATGTAC A		ATGCTAGTC
consensWesrPGI	ATCTTTTAC	AAACTGAA		TT TTCTACCGGG TCTGATGTAC A		ATGCTAGTC
consePGIintUNTR113	ATCTTTTAC	AAACTGAA		TT TTCTACCGGG TCTGATGTAC A		ATGCTAGTC
consePGIintUNTBrapaA	ATCTTTTAC	AAACTGAA		TT TTCTACCGGG TCTGATGTAC A		ATGCTAGTC
ConsePGIintUNTRRH1	ATCTTTTAC	AAACTGAA		TT TTCTACCGGG TCTGATGTAC A		ATGCTAGTC
PGIBo-EM:AF258277	ATCTTTTAC	AAACTGAA		TT TTCTACCGGG TCTGATGTAC A		ATGCTAGTC
PGIBra-EM:AF258278	ACCTTTTAC	AAACTGAA		AT GTCTACCGGG TCTGATGTAC A		ATGCTAGTC
consePGIintUNTBolera	ATCTTTTAC	AAACTGAA		TT TTCTACCGGG TCTGATGTAC A		ATGCTAGTC
consePGIintUNTR2000	ATCTTTT.AC	AAACTGAA		TT TTCTACCGGG TCTGATGTAC A		ATGCTAGTC
Consensus	atctttttac	aaactgaa		tt ttctaccggg tctgatgtac a		atgctAGTC

Figure 14 (a)

201	PGI int U --->		250
consePGIintUNTDrakka	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
consensWesrPGI	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTR113	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTBrapaA	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
ConsePGIintUNTRRH1	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
PGIBo-EM:AF258277	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
PGIBra-EM:AF258278	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTBolera	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
consePGIintUNTR2000	CTGT	CAGCAC TAATCTTGC GGTATG	AATT TGTGATTAAA TTTGTTTGTT
Consensus		ctgtcagcac taatcttgc ggtatg aatt tgtgattaaa tttgtttgt	
		ε	ε3
		251	300
consePGIintUNTDrakka	TGTGACTCTT	T.CTTCATTG TTCGTTTTCG TACAATAAAC	CGAATGTATA
consensWesrPGI	TGTGACTCTT	T.CTTCATTG TTCGTTTTCG TACAATAAAC	CGAATGTATA
consePGIintUNTR113	TGCGACTCTT	T.CTTCATTG TTCGTTTTCG TACAATAAAC	..AATGTATA
consePGIintUNTBrapaA	TGCGACTCTT	T.CTTCATTG TTCGTTTTCG TACAATAAAC	..AATGTATA
ConsePGIintUNTRRH1	TGCGACTCTT	T.CTTCATTG TTCGTTTTCG TACAATAAAC	..AATGTATA
PGIBo-EM:AF258277	TGTGACTCTT	T.CTTCATTG TTCGTTTTCG TACAATAAAC	CGAATGTATA
PGIBra-EM:AF258278	TGTGACTCTT	TTCTTCATTG TTCGTTTTCG TACAATAAAC	CGAATGTATA
consePGIintUNTBolera	TG.GACTCTT	T.CTTCATTG TTCGTTTTCG TACAATAAAC	CGAATGTATA
consePGIintUNTR2000	TGTGACTCTT	T.CTTCATTG TTCGTTTTCG TACAATAAAC	CGAATGTATA
Consensus	tg.gactcctt	t.cttcattg ttcgttttcg tacaataaac	CGaatgtata
		ε	ε3
		301	<--- PGIol antL 341 350
consePGIintUNTDrakka	ATCTTTTTTAC	AAACTGAA TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consensWesrPGI	ATCTTTTTTAC	AAACTGAA TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTR113	ATCTTTTTTAC	AAACTGAA TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTBrapaA	ATCTTTTTTAC	AAACTGAA TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
ConsePGIintUNTRRH1	ATCTTTTTTAC	AAACTGAA TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
PGIBo-EM:AF258277	ATCTTTTTTAC	AAACTGAA TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
PGIBra-EM:AF258278	ACCTTTTTTAC	AAACTGAA AT GTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTBolera	ATCTTTTTTAC	AAACTGAA TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
consePGIintUNTR2000	ATCTTTT.AC	AAACTGAA TT TTCTACCGGG TCTGATGTAC A	ATGCTAGTC
Consensus	atcttttttac	aaactgaa tt ttctaccggg tctgatgtac a	atgctAGTC
		ε	
		351	400
consePGIintUNTDrakka	TCCATGTTCT	TGGGGATCAT GATTTATTTT CTACATGTAT	TCAGACAGTA
consensWesrPGI	TCCATGTTCT	TGGGGATCAT GATTTATTTT CT.CATGTAT	TCAGACAGTA
consePGIintUNTR113	TCCATGTTCT	TGGGGATCAT GATTTATTTT CTACATGTGT	TCAGCCAGTA
consePGIintUNTBrapaA	TCCATGTTCT	TGGGGATCAT GATTTATTTT CTACATGTGT	TCAGCCAGTA
ConsePGIintUNTRRH1	TCCATGTTCT	TGGGGATCAT GATTTATTTT CTACATGTGT	TCAGCCAGTA
PGIBo-EM:AF258277	TCCATGTTCT	TGGGGATCAT GATTTATTTT CTACATGTAT	TCAGACAGTA
PGIBra-EM:AF258278	TCCATGTTCT	TGGGGATCAT GATTTATTTT CTACATGTAT	TCAGACAGTA
consePGIintUNTBolera	TCCATGTTCT	TGGGGATCAT GATTTATTTT CTACATGTAT	TCAGACAGTA
consePGIintUNTR2000	TCCATGTTCT	TGGGGATCAT GATTTATTTT CTACATGTAT	TCAGACAGTA
Consensus	TCCATGTTCT	TGGGGATCAT GATTTATTTT CTaCATGTAT	TCAGACAGTA
		ε5	ε6
		401	450
consePGIintUNTDrakka	CAGAAGAAAG	TGTTTAAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
consensWesrPGI	CAGAAGAAAG	TGTTTAAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
consePGIintUNTR113	CAGAAGAAAG	TGTTTAAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
consePGIintUNTBrapaA	CAGAAGAAAG	TGTTTAAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
ConsePGIintUNTRRH1	CAGAAGAAAG	TGTTTAAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
PGIBo-EM:AF258277	CAGAAGAAAG	TATTTAAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
PGIBra-EM:AF258278	CAGAAGAAA	TGTTTAAAAC TCTGGATGTT TTGATTTACA	GTTAGTGGAG
consePGIintUNTBolera	CAGAAGAAAG	TGTTTAAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
consePGIintUNTR2000	CAGAAGAAAG	TGTTTAAAAC TCTGGATGTT TTAATTTACA	GTTAGTGGAG
Consensus	CAGAAGAAg	TgTTTAAAAC TCTGGATGTT TTaATTTACA	GTTAGTGGAG
		ε7	ε

Figure 14 (b)

	451	end of Data Base PGI sequences				500
consePGIintUNTDrakka	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
consensWesrPGI	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
consePGIintUNTR113	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
consePGIintUNTBrapaA	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
ConsePGIintUNTRRH1	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
PGIBo-EM:AF258277	AAGTTCGGCA	TTGATCC...	
PGIBra-EM:AF258278	AAGTTCGGCA	TTGATCCGAA	CAA.....	
consePGIintUNTBolera	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
consePGIintUNTR2000	AAGTTCGGCA	TTGATCCGAA	CAATGCATTT	GCATTTTGGG	ACTGGGTTGG	
Consensus	AAGTTCGGCA	TTGATCCgaa	caatgcattt	gcattttggg	actggggttgg	
	501					550
consePGIintUNTDrakka	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCG	
consensWesrPGI	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCG	
consePGIintUNTR113	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCA	
consePGIintUNTBrapaA	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCA	
ConsePGIintUNTRRH1	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCA	
PGIBo-EM:AF258277	
PGIBra-EM:AF258278	
consePGIintUNTBolera	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCG	
consePGIintUNTR2000	TGGAAGGTAC	AGTGGTAAGT	GCTTGTTTAT	TTGGTTGTAT	TAATTTCTCG	
Consensus	tggaaggtac	agtggtaagt	gcttgtttat	ttggttgtat	taatttctc	
						8 9
	551					600
consePGIintUNTDrakka	TCCATTTCCG	CTTGCTTAGT	GTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
consensWesrPGI	TCCATTTCCG	CTTGCTTAGT	GTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
consePGIintUNTR113	TCCATATCCG	CTTGCTTAGT	TTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
consePGIintUNTBrapaA	TCCATATCCG	CTTGCTTAGT	TTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
ConsePGIintUNTRRH1	TCCATATCCG	CTTGCTTAGT	TTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
PGIBo-EM:AF258277	
PGIBra-EM:AF258278	
consePGIintUNTBolera	TCCATTTCCG	CTTGCTTAGT	GTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
consePGIintUNTR2000	TCCATTTCCG	CTTGCTTAGT	GTATAACTGA	AATTCTTTTG	CAGTTTGCAG	
Consensus	tccat.tccg	cttgcttagt	.tataactga	aattcttttg	cagtttgcag	
	10		11			
	601					650
consePGIintUNTDrakka	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCTGTGGTTG	
consensWesrPGI	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCTGTGGTTG	
consePGIintUNTR113	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCCGTGGTTG	
consePGIintUNTBrapaA	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCCGTGGTTG	
ConsePGIintUNTRRH1	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCCGTGGTTG	
PGIBo-EM:AF258277	
PGIBra-EM:AF258278	
consePGIintUNTBolera	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCTGTGGTTG	
consePGIintUNTR2000	TGCTGTTGGA	GTCTTACCAT	TGTCTCTACA	GTATGGCTTC	TCTGTGGTTG	
Consensus	tgctgttga	gtcttaccat	tgtctctaca	gtatggcttc	tc.tgtggttg	
						12
	651					700
consePGIintUNTDrakka	AGAAGTACGG	TACCTTCTAC	TTTATTAGCC	ATCTCATAAA	ATGTCTTAGG	
consensWesrPGI	AGAAGTACGG	TACCTTCTAC	TTTATTAGCC	ATCTCATAAA	ATGTCTTAGG	
consePGIintUNTR113	AGAAGTACGG	TACCTTCTAC	TTTATTAGCC	ATCTCATAAA	ATGTCTTAGG	
consePGIintUNTBrapaA	AGAAGTACGG	TACCTTCTAC	TTTATTAGCC	ATCTCATAAA	ATGTCTTAGG	
ConsePGIintUNTRRH1	AGAAGTACGG	TACCTTCTAC	TTTATTAGCC	ATCTCATAAA	ATGTCTTAGG	
PGIBo-EM:AF258277	
PGIBra-EM:AF258278	
consePGIintUNTBolera	AGAAGTACGG	TACCTTCTAC	TTTATTAGCC	ATCTCATAAA	A.GTCTTAGG	
consePGIintUNTR2000	AGAAGTACGG	TACCTTCTAC	TTTATTAGCC	ATCTCATAAA	ATGTCTTAGG	
Consensus	agaagtacgg	taccttctac	tttat.agcc	atctcataaa	atgtctt.gg	
			13			14

Figure 14 (c)

	701		750
consePGIintUNTDrakka	CATATTCTTT CTATTTTATT TTCCTCTTAA TGATTTCCTC TTTTTTTTAT		
consensWesrPGI	CATATTCTTT CTATTTTATT TTCCTCTTAA TGATTTCCTC TTTTTTTTAT		
consePGIintUNTR113	CATATTCTTT CTATTTTATT TTCCTCTGAA TGATTTCCTC TCTTTTAT..		
consePGIintUNTRapaa	CATATTCTTT CTATTTTATT TTCCTCTGAA TGATTTCCTC TCTTTTAT..		
ConsePGIintUNTRRH1	CATATTCTTT CTATTTTATT TTCCTCTGAA TGATTTCCTC TCTTTTAT..		
PGIBo-EM:AF258277		
PGIBra-EM:AF258278		
consePGIintUNTBolera	CATATTCTTT CTATTTTATT TTCCTCTTAA TGATTTCCTC TTTTTTTA..		
consePGIintUNTR2000	CATATTCTTT CTATTTTATT TCCCTCTTAA TGATTTCCTC TTTTTTTTAT		
Consensus	catattcttt ctattttatt ttcctctt aa tgatttcctc tttttt..	15	16 17
	751		800
consePGIintUNTDrakka	TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG		
consensWesrPGI	TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG		
consePGIintUNTR113	TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG		
consePGIintUNTRapaa	TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG		
ConsePGIintUNTRRH1	TGCATTCCCG TTTTATTTTC AAAAGTTGTC ACTGTCTCTA AATCAAGAAG		
PGIBo-EM:AF258277		
PGIBra-EM:AF258278		
consePGIintUNTBolera	TGCATTCCCG TTTTATTT.C AAAAGTTGTC CGGCCCCCTA AACCAAGAAG		
consePGIintUNTR2000	TGCATTCCCG TTTTATTTTC AAAAGTTGTT ACTGTCTCTA AATCAAGAAG		
Consensus	tgcatcccg ttttattttc aaaagttgt. actgtctcta aatcaagaag		
	801		850
consePGIintUNTDrakka	AAACCTTCTT AGTAGATCCA GTGATATTC AGCCTTTTCT AAATTGGACT		
consensWesrPGI	AAACCTTCTT AGTAGATCCA GTGATATTC AGCCTTTTCT AAATTGGACT		
consePGIintUNTR113	AAACCTTCTT AGTAGATCCA GTTGATATTC AGCCTTTTCT AAATTGGACT		
consePGIintUNTRapaa	AAACCTTCTT AGTAGATCCA G.TGATATTC AGCCTTTTCT AAATTGGACT		
ConsePGIintUNTRRH1	AAACCTTCTT AGTAGATCCA GTTGATATTC AGCCTTTTCT AAATTGGACT		
PGIBo-EM:AF258277		
PGIBra-EM:AF258278		
consePGIintUNTBolera	AAACCTTTCT AGGA...CCA GA....CTCC ACCCTTTTCT AAATTGGACT		
consePGIintUNTR2000	AAACCTTCTT AGTAGATCCA GTGATATTC AGCCTTTTCT AAATTGGACT		
Consensus	aaaccttctt agtagatcca g.tgatattc agcctttt..t aaattggact	18	19
	851		900
consePGIintUNTDrakka	GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATAGCATT TCCAGTCCCC		
consensWesrPGI	GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATAGCATT TCCAGTCCAC		
consePGIintUNTR113	GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCC..		
consePGIintUNTRapaa	GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCC..		
ConsePGIintUNTRRH1	GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCCAC		
PGIBo-EM:AF258277		
PGIBra-EM:AF258278		
consePGIintUNTBolera	GCAGGTTTTT AAA.GGGGGC TTCAAGCATT GATAGCATT TCCAGTCCAC		
consePGIintUNTR2000	GCAGGTTTTT AAACGGGAGC TTCAAGCATT GATAGCATT TCCAGTCCAC		
Consensus	gcagggtttt aaa.gggagc ttcaagcatt gatlagcatt tccagtcc.c	20	
	901		950
consePGIintUNTDrakka	ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT GTGTGATTAT		
consensWesrPGI	ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT		
consePGIintUNTR113	.CCCGTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. .GTGATTAT		
consePGIintUNTRapaa	.CCCGTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT		
ConsePGIintUNTRRH1	ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT		
PGIBo-EM:AF258277		
PGIBra-EM:AF258278		
consePGIintUNTBolera	ACCCGTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT		
consePGIintUNTR2000	ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT		
Consensus	acc.gtttga gaagaatata cccgtgagtt gcattagtt. gtgtgattat		

Figure 14 (d)

	951				1000
consePGIintUNTDrakka	ACAGTTTTTC	TTGTCTTTTT	GCTATGCCCA	TCAACACTAG	AAGATTCTGTG
consensWesrPGI	ACAGTTTT.C	TTGTCTTTTT.	GCTATGTCCA	TCAACACTAG	A.GATTCTGTG
consePGIintUNTR113	ACAGTTTT.C	TTGCCTTTTT	GCTAT..AGG	GCAAC.CTAG	A.GATTTCATG
consePGIintUNTBrapaA	ACAGTTTT.C	TTGTCTTTTT.	GCTATG.TCA	TCAAC.CTAG	A.GATTTCATG
ConsePGIintUNTRRH1	ACAGTTTT.C	TTGTCTTTTT	GCTAT...AT	GCAACCCTAG	..GATTTCATG
PGIBo-EM:AF258277
PGIBra-EM:AF258278
consePGIintUNTBolera	ACAGTTTT.C	TTGTCTTTTT	GCTAG..TGA	TCAAC.CTAG	A.GATTCTGTG
consePGIintUNTR2000	ACAGTTTT.C	TTGTCTTTTT	GCTATGTCCA	TCAACACTAG	A.GATTCTGTG
Consensus	acagtttt.c	ttgtcttttt	gctat....a	tcaac.ctag	a.gattcttg
					21

	1001				1050
consePGIintUNTDrakka	AAGTTATTAG	TGTAGCCAAC	GCCTAGGGGG	AGGTTGGTTG	GCTGTTTTGG
consensWesrPGI	AAGTTATTAG	TGTAGTCAAC	GCA.....
consePGIintUNTR113	AAGTTATTAG	TGTAGTCAAC	GCAGAGGAGA	G..TTCACTG	ACGG.....
consePGIintUNTBrapaA	AAGTTATTAG	TGTAGTCAAC	GCAGAGTGAG	AGG.TGATTG
ConsePGIintUNTRRH1	AAGTTATTAG	TGTAGTCAAC	GCAGAGGAGG	AGATGGTT..
PGIBo-EM:AF258277
PGIBra-EM:AF258278
consePGIintUNTBolera	AAGTTATTAG	TGTAGTCAAC	GCATAGGAGG	AGC.....
consePGIintUNTR2000	AAGTTATTAG	TGTAGTCAAC	GCATAGGGAG	AGGTGAT.GG	TGACTTTTGG
Consensus	aagttattag	tgtagtcaac	gca.agg.g.	.g.....

	1051		1076	
consePGIintUNTDrakka	ACGTTTTTCAC	GTGCTCCGGG	GGGTTTTTGG	GGACCAAACC
consensWesrPGI
consePGIintUNTR113
consePGIintUNTBrapaA
ConsePGIintUNTRRH1
PGIBo-EM:AF258277
PGIBra-EM:AF258278
consePGIintUNTBolera
consePGIintUNTR2000	ACGATTTCAG	GTGCTTTAGG	GTTATTG

Figure 15 (a)

	51		100
EMBH44836anti
GCP18-5CP418L-Sams
GCP18-2CP418L-Wes
GCP18-4CP418L-R2000	CP418L
conse129bal-Drak	AAACAAATCA	AAATTCTAAA TTTCTCCA
GCPS18-129Sam-ba2	AAAC TATGTA ACAAAATCA	AAATTGTAAA TTTCTCCA
GCPR18-3129R211-ba2	AA CCAAAATCC	AAATTGTAAA TTTCCCT.
GCP18-10129R20-ba2	CAAAATCCA	AAATTGTAAA TTTCT.CCT
Consensus
	101		150
EMBH44836anti
GCP18-5CP418L-Sams	AT	A.CATTTTCT GTAA
GCP18-2CP418L-Wes	AGG T.AT	A.CATTTTCT GTAA
GCP18-4CP418L-R2000	AGG TCAT	A.CATTTTCT GTAA
conse129bal-Drak	TCACAAGGAC	CTACAGAATA	GAGTTATCAT AACATTT CT GTAA
GCPS18-129Sam-ba2	TCGTAAAGAC	CTACAGAATA	GAGTTATCAT AACATTTCT G AA
GCPR18-3129R211-ba2	TGGTAAAGGC	CTCAAAAA.A	GAGGTATCAA AAC.TTTTCT GT.A
GCP18-10129R20-ba2	TGCTAAAGGC	C.CAAAA.A	AAGGT..CAA AACTT.TCCG GTAA
Consensus
	151		200
EMBH44836anti
GCP18-5CP418L-Sams	.TATTTCCAT CAAAATGA..	.CTAGAGAAC	AGCAGTTCTT ATAACATTAT
GCP18-2CP418L-Wes	.TATTTCCAT CAAAATGA..	.CTAGAGAAC	AG.AGTTCTT ATAACATTAT
GCP18-4CP418L-R2000	ATATTTCCAT CAAAATGA..	.CTAGAGAAC	AG.AGTTCTT ATAACATTAT
conse129bal-Drak	ATATTTCCAT CAAAATGA..	.CTAGAGAAC	AG.AGTTCTT ATAACATTAT
GCPS18-129Sam-ba2	ATGTTTCCAT CAAAATGA	CTATCGAAC	ATAATTAAT ATA.CATTTT
GCPR18-3129R211-ba2	ATGTTTCCAT CAAAATG.	CTATCGGAC	ATAATTAAT ATAAC.TTCT
GCP18-10129R20-ba2	ATGTTTCCAT CAAAATG.	CTTCGGA.C	ATAATTAAT ATAAC.TTCT
Consensus	ATGTTTCCCT CAAA.TGG	CTTCGGA.C	ATAATTAAT A...CATTTCT
	201		250
EMBH44836anti
GCP18-5CP418L-Sams	CTGTAAA TG.TTCCAA CAAAA CCACT	ACATAGCAGAGTTC	.TTATAACAT
GCP18-2CP418L-Wes	CTGTAAA TG.TTCCAA CAAAA CCACT	ACATAGCAGAGTTC	ATTATAACAT
GCP18-4CP418L-R2000	CTGTAAA TG.TTCCAA CAAAA CCACT	ACATAGCAGAGTTC	.TTATAACAT
conse129bal-Drak	CTGTAAA TG.TTCCAA CAAAA CCACT	ACATAGCAGAGTTC	.TTATAACAT
GCPS18-129Sam-ba2	CTG.AAAATATTCCCTCAAAAATT	.CATTT	ITC TTA.CAA.A.
GCPR18-3129R211-ba2	CTG.AAAATATTCCCTCAAAAATT	.CATTT	ITC T.ACAA.A.
GCP18-10129R20-ba2	CTG.AAA.TAATTCCCTCAAAAATT	.CATTT	ITC T.ACAA.A.
Consensus
	251		300
EMBH44836antiCTATACC
GCP18-5CP418L-Sams	TGTCTGT.AA ATGTCCAATC AAAACCACTA	CAGAACAAG	CTCCTATAAC
GCP18-2CP418L-Wes	TGTCTGT.AA ATGTCCAATC AAAACCACTA	CAGAACAAG	CTCCTATAAC
GCP18-4CP418L-R2000	TGTCTGT.AA ATGTCCAATC AAAACCACTA	CAGAACAAG	CTCCTATAAC
conse129bal-Drak	TGTCTGT.AA ATGTCCAATC AAAACCACTA	CAGAACAAG	CTCCTATAAC
GCPS18-129Sam-ba2	TGTTTC.....	CATCAAAATG	AGACTCA.G
GCPR18-3129R211-ba2	TGTTTC.....	CATCAAAATG	AGACTCA.G
GCP18-10129R20-ba2	TGTTTC.....	CATCAAAATG	AGACTCA.G
Consensus	tttctgt.aa tgtttccatc aaaatgacta	tccaacataa	ttaatataac
	301		350
EMBH44836anti	A TTGTTT ATACAAAGTT TCACT AAAT	CTACAAACTT	CCCCCGTAAA
GCP18-5CP418L-Sams	A TTGTTT ATACAAAGTTT .CACT AAAT	CTACAAACTT	TCCCGGTAAA
GCP18-2CP418L-Wes	A TTGTTT ATACAAAGTT TCACT AAAT	CTACAAACTT	TCCCGGTAAA
GCP18-4CP418L-R2000	A TTGTTT ATACAAAGTTT .CACT AAAT	CTACAAACTT	TCCCGGTAAA
conse129bal-Drak	A TTGTTT ATACAAAGTT TCACT AAAT	CTACAAACTT	TCCCGGTAAA
GCPS18-129Sam-ba2	AAC.CAGTTC TTGCAATAGTT	TCACTTAAAT	CTACAAACTT TC.....
GCPR18-3129R211-ba2	AACACAGTTC TTGCAATAGTT	TCACT.AAAT	CTACAAACTT TC.....
GCP18-10129R20-ba2	A.CCCAGTTC TTGCAATAGTT	TC.CT.AAAT	CTTCAAACTT TC.....
Consensus

Figure 15 (b)

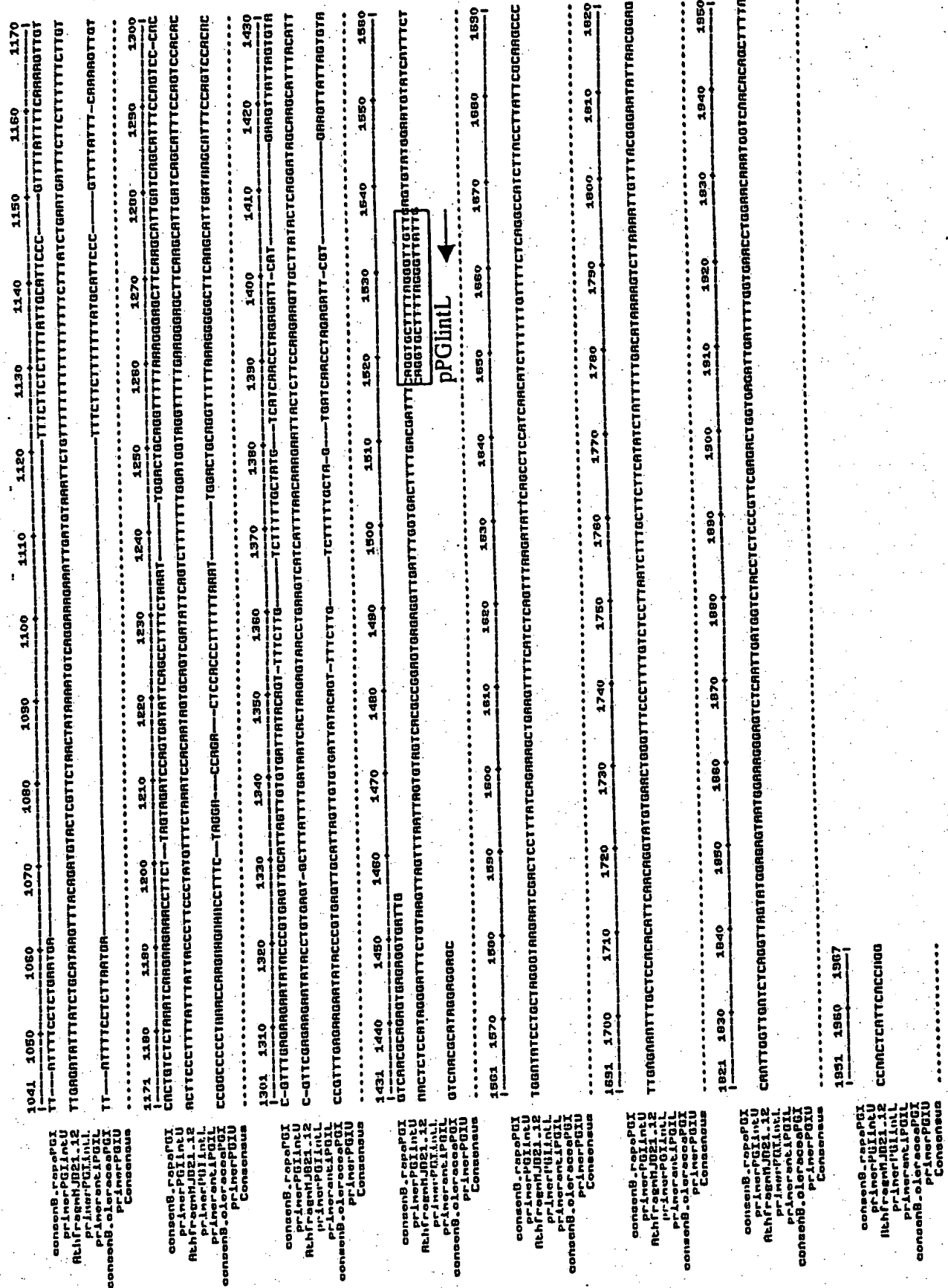
	351		400
EMB44836anti	351		
GCP18-5CP418L-Sams	351		
GCP18-2CP418L-Wes	351		
GCP18-4CP418L-R2000	351		
conse129ba1-Drak	351		
GCP18-129Sam-ba2	351		
GCP18-3129R211-ba2	351		
GCP18-10129R20-ba2	351		
Consensus	351		
	401		
EMB44836anti	401		
GCP18-5CP418L-Sams	401		
GCP18-2CP418L-Wes	401		
GCP18-4CP418L-R2000	401		
conse129ba1-Drak	401		
GCP18-129Sam-ba2	401		
GCP18-3129R211-ba2	401		
GCP18-10129R20-ba2	401		
Consensus	401		
	431		480
EMB44836anti	431		
GCP18-5CP418L-Sams	431		
GCP18-2CP418L-Wes	431		
GCP18-4CP418L-R2000	431		
conse129ba1-Drak	431		
GCP18-129Sam-ba2	431		
GCP18-3129R211-ba2	431		
GCP18-10129R20-ba2	431		
Consensus	431		
	530		
EMB44836anti	530		
GCP18-5CP418L-Sams	530		
GCP18-2CP418L-Wes	530		
GCP18-4CP418L-R2000	530		
conse129ba1-Drak	530		
GCP18-129Sam-ba2	530		
GCP18-3129R211-ba2	530		
GCP18-10129R20-ba2	530		
Consensus	530		
	580		
EMB44836anti	580		
GCP18-5CP418L-Sams	580		
GCP18-2CP418L-Wes	580		
GCP18-4CP418L-R2000	580		
conse129ba1-Drak	580		
GCP18-129Sam-ba2	580		
GCP18-3129R211-ba2	580		
GCP18-10129R20-ba2	580		
Consensus	580		
	630		
EMB44836anti	630		
GCP18-5CP418L-Sams	630		
GCP18-2CP418L-Wes	630		
GCP18-4CP418L-R2000	630		
conse129ba1-Drak	630		
GCP18-129Sam-ba2	630		
GCP18-3129R211-ba2	630		
GCP18-10129R20-ba2	630		
Consensus	630		

Figure 15 (c)

	631		690
EMBH44836anti	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT
GCP18-5CP418L-Sams	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT
GCP18-2CP418L-Wes	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT
GCP18-4CP418L-R2000	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT
conse129ba1-Drak	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT
GCP18-129Sam-ba2	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT
GCP18-3129R211-ba2	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT
GCP18-10129R20-ba2	GGAGCGATGG	GAAAAGAGAG	TGGCACGATT
Consensus	ggagcg.tgg	.aaaagagag	tggcacgatt
	691		740
EMBH44836anti	AGAGGGTGGT	GGATAAACTC	GCGTATGATC
GCP18-5CP418L-Sams	AGAGGGTGGT	GGATAAACTC	GCGTATGATC
GCP18-2CP418L-Wes	AGAGGGTGGT	GGATAAACTC	GCGTATGATC
GCP18-4CP418L-R2000	AGAGGGTGGT	GGATAAACTC	GCGTATGATC
conse129ba1-Drak	AGAGGGTGGT	GGATAAACTC	GCGTATGATC
GCP18-129Sam-ba2	AGAGGGTGGT	GGATAAACTC	GCGTATGATC
GCP18-3129R211-ba2	AGAGGGTGGT	GGATAAACTC	GCGTATGATC
GCP18-10129R20-ba2	AGAGGGTGGT	GGATAAACTC	GCGTATGATC
Consensus	agaggggtggt	ggataaaactc	gcgtatgatac
	741		790
EMBH44836anti	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG
GCP18-5CP418L-Sams	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG
GCP18-2CP418L-Wes	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG
GCP18-4CP418L-R2000	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG
conse129ba1-Drak	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG
GCP18-129Sam-ba2	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG
GCP18-3129R211-ba2	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG
GCP18-10129R20-ba2	TGCCGCCATT	TTTTTTGTCA	GGGCGCTCTG
Consensus	tgccgccatt	.tt.....c.	.gg.gc.c.g
	791		800
EMBH44836anti	TCAATGAAC	A	GTGACACGAC
GCP18-5CP418L-Sams	TCAATGAAC	AGAAT...	TC CGGG...
GCP18-2CP418L-Wes	CCAATGAACA	AGATTATTTT	CGATG..
GCP18-4CP418L-R2000
conse129ba1-Drak

[illegible]

Figure 16^{BIS}



Hipsflt162850ant1
 Seqqfc007190fln-AC011
 GCPATpboLJU
 Consensus

1 10 20 30 40 50 60 70 80 90 100 110 120 130
TTTGGTTGGTCTCACAGCTTTACTATTTCTTTCTTTGTTCTCTGATGGTGGAGTGGAAATATGAGCCGATCAATTATCGCTTGTCTGTTGATGTGTTGATGACCAAAACATCTCGGTTTATGAT
TGGTCTCAGCAGCTTTACTATTTCTTTCTTTGTTCTCTGATGGTGGAGTGGAAATATGAGCCGCTCAATTATCGCTTGTCTGATGTGTTGATGACCAAAACATCTCGGTTTATGAT

Consensus

N1psAt162850ant1
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 Consensus

[illegible]

Consensus

<https://doi.org/10.1016/j.jm.2019.01.001>
 GCRAP801JU
 Consensus

[illegible]

Consensus

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 GCPAtpBoLJU
 Consensus

[illegible]

Consensus

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GCPATp8o1JU
Consensus

[illegible]

Conclusions

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 Consensus

[illegible]

Consensus

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 Consensus

[illegible]

Consensus

HipsAt162850ant1
 eqAc007190fin-AC011
 GCPATpBo1JU
 Consensus

111 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200 2210 2220 2230 2240 2250 2260 2270 2280 2290 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400 2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520 2530 2540 2550 2560 2570 2580 2590 2600 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800 2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190 3200 3210 3220 3230 3240 3250 3260 3270 3280 3290 3300 3310 3320 3330 3340 3350 3360 3370 3380 3390 3400 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960 3970 3980 3990 4000 4010 4020 4030 4040 4050 4060 4070 4080 4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200 4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320 4330 4340 4350 4360 4370 4380 4390 4400 4410 4420 4430 4440 4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560 4570 4580 4590 4600 4610 4620 4630 4640 4650 4660 4670 4680 4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 4960 4970 4980 4990 5000 5010 5020 5030 5040 5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160 5170 5180 5190 5200 5210 5220 5230 5240 5250 5260 5270 5280 5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400 5410 5420 5430 5440 5450 5460 5470 5480 5490 5500 5510 5520 5530 5540 5550 5560 5570 5580 5590 5600 5610 5620 5630 5640 5650 5660 5670 5680 5690 5700 5710 5720 5730 5740 5750 5760 5770 5780 5790 5800 5810 5820 5830 5840 5850 5860 5870 5880 5890 5900 5910 5920 5930 5940 5950 5960 5970 5980 5990 6000 6010 6020 6030 6040 6050 6060 6070 6080 6090 6100 6110 6120 6130 6140 6150 6160 6170 6180 6190 6200 6210 6220 6230 6240 6250 6260 6270 6280 6290 6300 6310 6320 6330 6340 6350 6360 6370 6380 6390 6400 6410 6420 6430 6440 6450 6460 6470 6480 6490 6500 6510 6520 6530 6540 6550 6560 6570 6580 6590 6600 6610 6620 6630 6640 6650 6660 6670 6680 6690 6700 6710 6720 6730 6740 6750 6760 6770 6780 6790 6800 6810 6820 6830 6840 6850 6860 6870 6880 6890 6900 6910 6920 6930 6940 6950 6960 6970 6980 6990 7000 7010 7020 7030 7040 7050 7060 7070 7080 7090 7100 7110 7120 7130 7140 7150 7160 7170 7180 7190 7200 7210 7220 7230 7240 7250 7260 7270 7280 7290 7300 7310 7320 7330 7340 7350 7360 7370 7380 7390 7400 7410 7420 7430 7440 7450 7460 7470 7480 7490 7500 7510 7520 7530 7540 7550 7560 7570 7580 7590 7600 7610 7620 7630 7640 7650 7660 7670 7680 7690 7700 7710 7720 7730 7740 7750 7760 7770 7780 7790 7800 7810 7820 7830 7840 7850 7860 7870 7880 7890 7900 7910 7920 7930 7940 7950 7960 7970 7980 7990 8000 8010 8020 8030 8040 8050 8060 8070 8080 8090 8100 8110 8120 8130 8140 8150 8160 8170 8180 8190 8200 8210 8220 8230 8240 8250 8260 8270 8280 8290 8300 8310 8320 8330 8340 8350 8360 8370 8380 8390 8400 8410 8420 8430 8440 8450 8460 8470 8480 8490 8500 8510 8520 8530 8540 8550 8560 8570 8580 8590 8600 8610 8620 8630 8640 8650 8660 8670 8680 8690 8700 8710 8720 8730 8740 8750 8760 8770 8780 879

ໂຕກຳລັງ

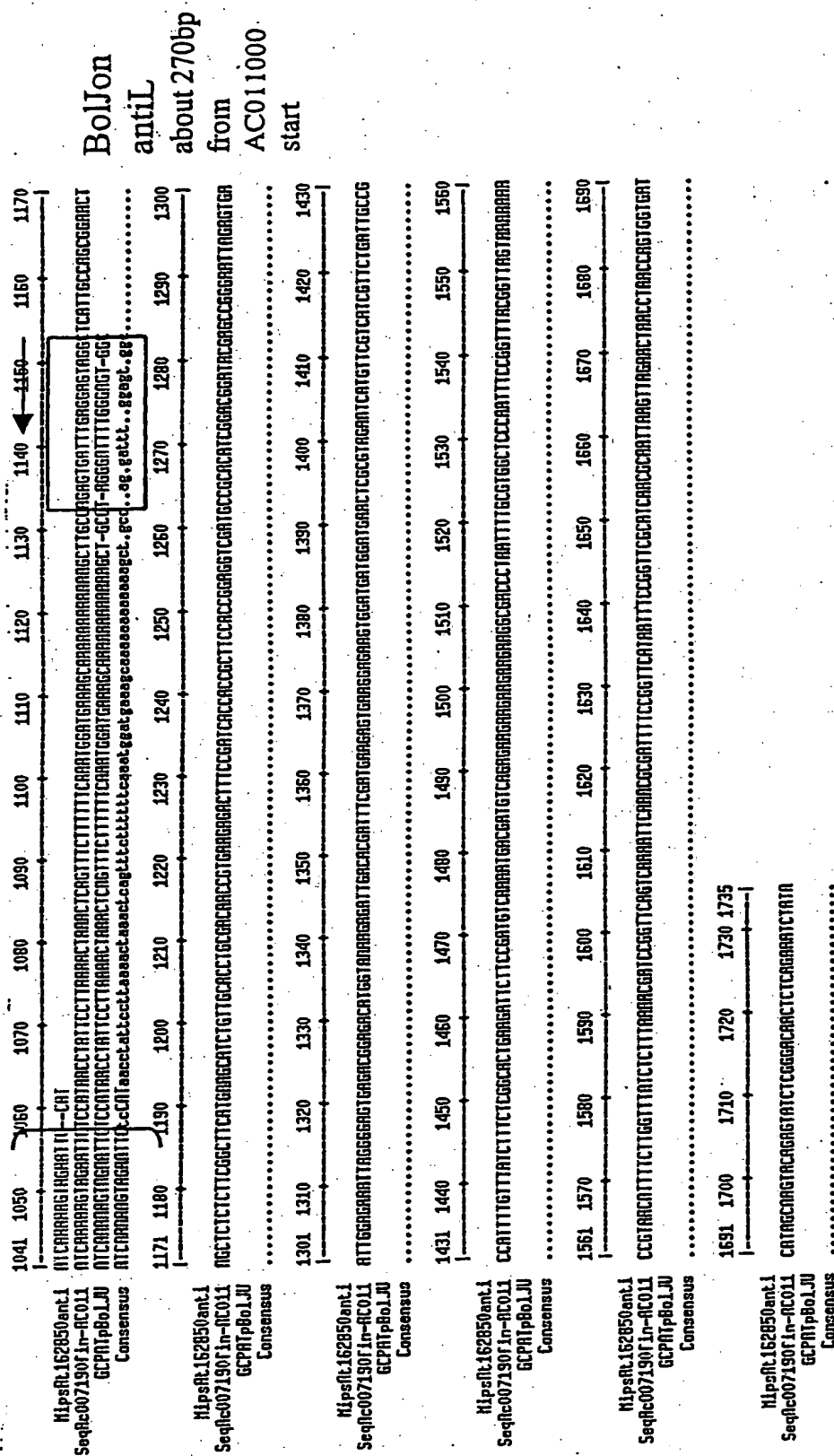
BolJon U
about 700bp
from AC007190
end

AC011000 start

overlapping

AC007190 end

Figure 17 ^{BIS}



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